CLAIMS

What we claim is:

1. A method for identifying a compound capable of modulating the hydrolase activity of a CLCA protein which method comprises:
   (a) subjecting one or more test compounds to a screen comprising at least one protein selected from the group consisting of: a CLCA protein or a fragment thereof; a homologue of a CLCA protein or a fragment thereof; and
   (b) measuring the hydrolase activity of the CLCA protein or homologue or fragment; and
   (c) comparing the measured hydrolase activity with the hydrolase activity of the CLCA protein or homologue or fragment in the absence of the test compound.

2. A method as claimed in claim 1 wherein at least one of the proteins is selected from the group consisting of: a mammalian CLCA protein or a fragment thereof; a homologue of a mammalian CLCA protein or a fragment thereof.

3. A method as claimed in claim 2 wherein at least one of the proteins is selected from the group consisting of: a human CLCA protein or a fragment thereof; a homologue of a human CLCA protein or a fragment thereof.

4. A method as claimed in claim 3 wherein at least one of the proteins is selected from the group consisting of: hCLCA1 or a fragment thereof; a homologue of hCLCA1 or a fragment thereof.

5. A method as claimed in claim 1 wherein the CLCA protein or fragment thereof or the homologue of a CLCA protein or fragment thereof is present as a fusion protein.

6. A method to design a compound capable of modulating CLCA hydrolase activity which comprises molecular modelling based on the interaction of a potential modulator with a hydrolase domain of a CLCA protein or homologue or fragment of either, wherein the three-dimensional structure of the hydrolase domain is defined by the set of atomic coordinates shown in Table 1.

7. A method to design a compound capable of modulating CLCA hydrolase activity which comprises molecular modelling based on the interaction of a potential modulator with the active site of a hydrolase domain of a CLCA protein or homologue or fragment of either, wherein the three-dimensional structure of the hydrolase domain is defined by the set of atomic coordinates shown in Table 1 and the active site comprises the amino acid residues within 15Å of atom Zn-1300 in the set of atomic coordinates shown in Table 1.

8. A method for *in silico* screening for a compound capable of modulating CLCA hydrolase activity which comprises

   a) searching a structural database of compounds; and

   b) selecting a compound structure that may interact with a hydrolase domain of a CLCA protein or homologue or fragment of either, wherein the three-dimensional structure of the hydrolase domain is defined by the set of atomic coordinates shown in Table 1.

9. A method for *in silico* screening for a compound capable of modulating CLCA hydrolase activity which comprises

   a) searching a structural database of compounds; and

   b) selecting a compound structure that may interact with the active site of a hydrolase domain of a CLCA protein or homologue or fragment of either, wherein the three-dimensional structure of the hydrolase domain is defined by the set of

atomic coordinates shown in Table 1 and the active site comprises the amino acid residues within 15Å of atom Zn-1300 in the set of atomic coordinates shown in Table 1.

10. A method for designing an antibody capable of modulating the hydrolase activity of a CLCA protein which method comprises using the three-dimensional structure of a CLCA hydrolase domain to identify suitable epitopes in the vicinity of the active site, wherein the three-dimensional structure of the hydrolase domain is defined by the set of atomic coordinates shown in Table 1 and the active site comprises the amino acid residues within 15Å of atom Zn-1300 in the set of atomic coordinates shown in Table 1.

11. A method as claimed in claim 10 wherein the epitopes include only surface residues within 15Å of atom Zn-1300 in the set of atomic coordinates shown in Table 1.